

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: March 14, 2003, 04:41:21 ; Search time 19.3258 seconds  
(without alignments)  
553.709 Million cell updates/sec

Title: US-09-698-781-3

Perfect score: 1436

Sequence: 1 MKQILHPALETATLTPVL.....KHQLVDRSCAKSCNSNSIY 258

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1363	94.9	245	1	CRS3_HUMAN
2	988	68.8	243	1	TPX1_HUMAN
3	968.5	67.4	244	1	TPX1_CAVPO
4	929	64.7	245	1	CRS3_HORSE
5	830	57.8	243	1	TPX1_MOUSE
6	766.5	53.4	244	1	AEGL_MOUSE
7	755.5	52.6	246	1	AEGL_RAT
8	717.5	46.8	242	1	HELO_HELMO
9	617.5	43.0	241	1	AEGL_MOUSE
10	552	38.4	183	1	CRVP_TRIMU
11	529.5	36.9	249	1	CRS1_HUMAN
12	328	22.8	266	1	GLIP_HUMAN
13	274	19.1	424	1	ASP_ANCCA
14	269	18.7	202	1	VAS1_VESCR
15	265	18.5	202	1	VAS2_VESCR
16	259	18.0	227	1	VAS2_DOLMA
17	257.5	17.9	211	1	VAS3_SOLRI
18	234	17.7	203	1	VAS3_DOLAR
19	232.5	17.6	215	1	VAS3_DOLMA
20	251	17.5	312	1	YR81_CAEEL
21	250.5	17.4	204	1	VAS_VESFL
22	250.5	17.4	205	1	VAS_VESFO
23	250.5	17.4	227	1	VAS_VESYU
24	248	17.3	234	1	VAS3_SOLIN
25	245.5	17.1	204	1	VAS_VESGE
26	243.5	17.0	204	1	VAS_VESMA
27	243	16.9	202	1	VAS_VESMA
28	241.5	16.8	204	1	VAS_VESPE
29	240.5	16.7	206	1	VAS_VESYU
30	228.5	15.9	164	1	PR13_HORVU
31	227.5	15.8	164	1	PR1_HORVU
32	222.5	15.5	206	1	VAS3_POLDO
33	222	15.5	205	1	VAS3_POLEX

## ALIGNMENTS

```

RESULT 1
CRS3_HUMAN
ID CRS3_HUMAN STANDARD: PRT: 245 AA.
AC PS4108: 015512:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cysteine-rich secretory protein-3 precursor (CRISP-3) (SGP28 protein).
GN CRISP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RX MEDLINE=96270732; PubMed=8665901;
RA Kraetzschmar J., Haendler B., Eberspaecher U., Roostermann D.,
RA Donner P., Schleuning W.-D.;
RT "The human cysteine-rich secretory protein (CRISP) family. Primary
RT structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3.";
RL Eur. J. Biochem. 236:827-836(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96186934; PubMed=8601434;
RA Kjeldsen L., Cowland J.B., Johnson A.H., Borregaard N.;
RT "SGP28, a novel matrix glycoprotein in specific granules of human
RT neutrophils with similarity to a human testis-specific gene product
RT and a rodent sperm-coating glycoprotein.";
RL FEBS Lett. 380:246-250(1996).
CC -1- SUBCELLULAR LOCATION: SECRETED; IN NEUTROPHILS, LOCALIZED IN
CC SPECIFIC GRANULES.
CC -1- TISSUE SPECIFICITY: SALIVARY GLAND, PANCREAS AND PROSTATE >
CC EPIDIDYMIS, OVARY, THYMUS AND COLON.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
-----
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-----
CC EMBL: X95240; CAAG4527.1; -
CC EMBL: X94323; CAAG3984.1; -
CC HSSP: P04284; ICEE.
CC InterPro: IPR001283; Allrgn_V5/TPx1.
CC Pfam: PF00188; SCP_1.
CC PRINTS: PR00837; V5PPLIKE.
CC PRODOM: PD000542; Allrgn_V5/TPx1_1.
CC SMART: SM00198; SCP_1.
CC PROSITE: PS01009; SCP_AG5_PRL_SC7_1; 1.
CC PROSITE: PS01010; SCP_AG5_PRL_SC7_2; 1.
CC GlycoProtein: Signal; Multigene family; Polymorphism.
CC SIGNAL 1 20 POTENTIAL.

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FT CHAIN 21 245 CYSTEINE-RICH SECRETORY PROTEIN-3.
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 106 106 S -> P (IN DBSNP:495335).
FT VARIANT 134 134 /FTID-VAR-011718.
FT VARIANT 134 134 A -> S (IN DBSNP:1864312).
FT SEQUENCE 245 AA: 27630 MM: B4DD79CB7AE9E5F9 CRC64:
SQ
Query Match 94.9%; Score 1363; DB 1; Length 245;
Best Local Similarity 99.6%; Pred. No. 2.2e-109;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 MTEPVLFLVAGLPSFPANEDKPAFTALLTQTQVOREIVYKHNELRRVSPARM 73
DB 1 MTEPVLFLVAGLPSFPANEDKPAFTALLTQTQVOREIVYKHNELRRVSPARM 60
QY 74 LKHEMNKEAANAKMANOCNRYRHSNPKDRMTSLKCGENLYMSSAPSSWSOAIOSWFDEY 133
DB 61 LKHEMNKEAANAKMANOCNRYRHSNPKDRMTSLKCGENLYMSSAPSSWSOAIOSWFDEY 120
QY 134 NDEDFGVGPKTPNAVGHYTVQVWYSSYLVCGNAYCPNOKVLKYYVCOYCPAGNMNR 193
DB 121 NDEDFGVGPKTPNAVGHYTVQVWYSSYLVCGNAYCPNOKVLKYYVCOYCPAGNMNR 180
QY 194 LYVPEEGAPCASPDCDGLCTNGCKYEDLYSNCKSLKLTLLCKHQLVRSCKASCNC 253
DB 181 LYVPEEGAPCASPDCDGLCTNGCKYEDLYSNCKSLKLTLLCKHQLVRSCKASCNC 240
QY 254 SNSIY 258
DB 241 SNSIY 245

RESULT 2
TPX1_HUMAN
ID TPX1_HUMAN STANDARD; PRT; 243 AA.
AC P16562;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Testis-specific protein TPX-1 precursor (Cysteine-rich secretory
DE protein-2) (Crisp-2).
GN TPX1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RA MEDLINE=96270732; PubMed=8665901;
RA Kraetzschmar J., Haendler B., Eberspaecher U., Roostermann D.,
RA Donner P., Schleuning W.-D.;
RT "The human cysteine-rich secretory protein (CRISP) family. Primary
RT structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3.";
RL Eur. J. Biochem. 236:827-836(1996).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: TESTIS AND EPIDIDYMIS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AGS; FUNGI SC7/SC14 AND PLANTS PR-1.
CC
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CC -----
DR EMBL: M25532; AAA61220.1; -
DR EMBL: X95239; CAA64526.1; -
DR PIR: B33329; B33329.
DR Genew; HGNC:12024; TPX1.
DR MIM: 187430; -
DR InterPro: IPR001283; Allrgn_V5/TPX1.
DR Pfam: PF00188; SCP_1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/TPX1; 1.
DR SMART: SM00198; SCP_1.
DR PROSITE: PS01009; SCP_AGS_PRL_SG7_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SG7_2; 1.
KW Testis; signal; Multigene family.
FT SIGNAL 1 21
FT CHAIN 22 243
FT SEQUENCE 243 AA: 27259 MM: C5FE698C449CFAD9 CRC64:
SQ
Query Match 68.8%; Score 988; DB 1; Length 243;
Best Local Similarity 71.8%; Pred. No. 2.2e-77;
Matches 176; Conservative 25; Mismatches 42; Indels 2; Gaps 2;

QY 14 MTEPVLFLVAGLPSFPANEDKPAFTALLTQTQVOREIVYKHNELRRVSPARM 73
DB 1 MALLPV-LFLVTVLPSLPA-EGKDPAFALLTQTQVOREIVYKHNELRRVSPARM 58
QY 74 LKHEMNKEAANAKMANOCNRYRHSNPKDRMTSLKCGENLYMSSAPSSWSOAIOSWFDEY 133
DB 59 LKHEMSREVTNMAQMANKCTLOHSDPEDKRTSRCEENLYMSDPSWSAIOISWDEI 118
QY 134 NDEDFGVGPKTPNAVGHYTVQVWYSSYLVCGNAYCPNOKVLKYYVCOYCPAGNMNR 193
DB 119 LDFYGVGPKSPNNAVGHYTVQVWYSSYLVCGNAYCPNOKVLKYYVCOYCPAGNMNR 178
QY 194 LYVPEEGAPCASPDCDGLCTNGCKYEDLYSNCKSLKLTLLCKHQLVRSCKASCNC 253
DB 179 KNTPEQGTGTCACGPDGDLCTNSCQYODLNSCDLSKNTAGCEHELLKCKKATCTLC 238
QY 254 SNSIY 258
DB 239 ENKIY 243

RESULT 3
TPX1_CAVPO
ID TPX1_CAVPO STANDARD; PRT; 244 AA.
AC O60477;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Testis-specific protein TPX-1 precursor (Autoantigen 1) (25 kDa
DE acrosomal autoantigen) (AA1).
GN TPX1.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Testis;
RA MEDLINE=96354287; PubMed=9115720;
RA Foster J.A., Gerton G.L.;
RT "Autoantigen 1 of the guinea pig sperm acrosome is the homologue of
RT mouse Tpx-1 and human TPX1 and is a member of the cysteine-rich
RT secretory protein (CRISP) family.";
RL Mol. Reprod. Dev. 44:221-229(1996).
CC (2)
CC SEQUENCE OF 22-41.
CC MEDLINE=88193219; PubMed=3282555;
CC Hardy D.M., Huang T.T.F. Jr., Driscoll W.J., Tung K.S.K., Wild G.C.;

```

RT "Purification and characterization of the primary acrosomal  
 RL autoantigen of guinea pig epididymal spermatozoa."  
 CC Biol. Reprod. 38:423-437(1988).  
 CC -1- TISSUE SPECIFICITY: TESTIS  
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
 CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.  
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 CC -----  
 CC EMBL: U35712; AAC52616.1; -  
 CC InterPro: IPR001283; Allrgn\_V5/TPx1.  
 CC Pfam: PF00188; SCP; 1.  
 CC PRINTS: PR00837; V5TPXLIKE.  
 CC ProDom: PD000542; Allrgn\_V5/TPx1; 1.  
 CC SMART: SM00198; SCP; 1.  
 CC PROSITE: PS01009; SCP\_AGS\_PRL\_SC7\_1; 1.  
 CC PROSITE: PS01010; SCP\_AGS\_PRL\_SC7\_2; 1.  
 CC Testis: Signal.  
 CC KW Signal: Signal.  
 CC FT CHAIN 1 21  
 CC SIGNAL 1 21  
 CC SEQUENCE 244 AA: 27248 MW: 5808DE6EECE1A12 CRC64;  
 SQ  
 Query Match 67.4%; Score 968.5; DB 1; Length 244;  
 Best Local Similarity 70.2%; Pred. No. 1e-75;  
 Matches 172; Conservative 26; Mismatches 46; Indels 1; Gaps 1;  
 QY 14 MTLFVLLFLVAGLPSFPANEDKDPATLTTOTQVOREIYNKNELEBRASPPARRM 73  
 DB 1 MALLPVLFLVLAFLPFCVLTN-GKDPATLITTOQVONEIINKHNOAKRSTPPASNM 59  
 QY 74 LKEMNKKEAANAOKKAWANOCNRHSNPKDRMTSLKCGENLYSSAPSSMSQAIOGFDE 133  
 DB 60 LKEMNKKEAANAOKKAWANOCNRHSNPKDRMTSLKCGENLYSSAPSSMSQAIOGFDE 119  
 QY 134 NDEFGVGPKTPNAVYGHYTOVWYSSYVGGGNAYCPNOKYLKYYVGYOCPAGMANR 193  
 DB 120 QDFTGVGPKTPNAVYGHYTOVWYSSYVGGGNAYCPNOKYLKYYVGYOCPAGMANR 179  
 QY 194 RLVPPYEGAPCASPDCNDGDLCTNGCKYEDLYSNCKSLKLTLCRHOVLRDSCASCNC 253  
 DB 180 KNTPYKOGIPCARCPGNCNDGDLCTNGCKYEDLYSNCKSLKLTLCRHOVLRDSCASCNC 239  
 QY 254 SNSIT 258  
 DB 240 EDKIT 244

RESULT 4  
 CRS3 HORSE  
 ID CRS3 HORSE STANDARD; PRT: 245 AA.  
 AC 019010;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cysteine-rich secretory protein-3 precursor (CRISP-3).  
 GN CRISP3.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Amplified;  
 RX MEDLINE=98422318; PubMed=9748582;  
 RA Schambony A., Gentzel M., Wolfes H., Ralda M., Neumann U.,  
 RA Toepfer-Petersen E.;  
 RT "Equine CRISP-3: primary structure and expression in the male genital

RT tract."; Biophys. Acta 1387:206-216(1998).  
 RL Biochim. Biophys. Acta 1387:206-216(1998).  
 CC -1- SUBCELLULAR LOCATION: SECRETED; IN NEUTROPHILS, LOCALIZED IN  
 CC SPECIFIC GRANULES (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE SALIVARY GLAND, IN THE  
 CC AMPULLA AND THE SEMINAL VESICLE.  
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
 CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.  
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 CC -----  
 CC EMBL: AJ001400; CA04729.1; -  
 CC HSP: P04284; ICFE.  
 CC InterPro: IPR001283; Allrgn\_V5/TPx1.  
 CC Pfam: PF00188; SCP; 1.  
 CC PRINTS: PR00837; V5TPXLIKE.  
 CC ProDom: PD000542; Allrgn\_V5/TPx1; 1.  
 CC SMART: SM00198; SCP; 1.  
 CC PROSITE: PS01009; SCP\_AGS\_PRL\_SC7\_1; 1.  
 CC PROSITE: PS01010; SCP\_AGS\_PRL\_SC7\_2; 1.  
 CC Signal: Multigene family.  
 CC FT CHAIN 1 22  
 CC SIGNAL 1 22  
 CC SEQUENCE 245 AA: 27308 MW: 893A4E87F402BA22 CRC64;  
 SQ  
 Query Match 64.7%; Score 929; DB 1; Length 245;  
 Best Local Similarity 65.9%; Pred. No. 2.4e-72;  
 Matches 162; Conservative 33; Mismatches 49; Indels 2; Gaps 2;  
 QY 14 MTLFVLLFLVAGLPSFPANEDKDPATLTTOTQVOREIYNKNELEBRASPPARRM 73  
 DB 1 MALLPVLFLVLAFLPFCVLTN-GKDPATLITTOQVONEIINKHNOAKRSTPPASNM 59  
 QY 74 LKEMNKKEAANAOKKAWANOCNRHSNPKDR-MTSLKCGENLYSSAPSSMSQAIOGFDE 132  
 DB 60 LKEMNKKEAANAOKKAWANOCNRHSNPKDR-MTSLKCGENLYSSAPSSMSQAIOGFDE 119  
 QY 133 YNDFGVGPKTPNAVYGHYTOVWYSSYVGGGNAYCPNOKYLKYYVGYOCPAGMANR 192  
 DB 120 VDFEFGVGPKTPNAVYGHYTOVWYSSYVGGGNAYCPNOKYLKYYVGYOCPAGMANR 179  
 QY 193 RLVPPYEGAPCASPDCNDGDLCTNGCKYEDLYSNCKSLKLTLCRHOVLRDSCASCNC 252  
 DB 180 KNTPYKOGIPCARCPGNCNDGDLCTNGCKYEDLYSNCKSLKLTLCRHOVLRDSCASCNC 239  
 QY 253 CSNSIT 258  
 DB 240 CENKIT 245

RESULT 5  
 TPX1 MOUSE  
 ID TPX1 MOUSE STANDARD; PRT: 243 AA.  
 AC P16563;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Testis-specific protein TPX-1 precursor.  
 GN TPX1 OR TPX-1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=90129048; PubMed=2613236;

```

RA Kasahara M., Gutknecht J., Brew K., Spurr N., Goodfellow P.N.;
RT "Cloning and mapping of a testis-specific gene with sequence
RL similarity to a sperm-coating glycoprotein gene."
CC Genomics 5:527-534(1989).
CC -1- SUBCELLULAR LOCATION: secreted (Probable).
CC -1- TISSUE SPECIFICITY: TESTIS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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CC -----
CC EMBL: M25533; AAA0472.1; -.
CC PIR: A33329; A33329.
CC HSSP: P04284; ICPE.
CC MGD: MGI:98815; Tpx1.
CC InterPro: IPR001283; Allrgn_V5/TPx1.
CC Pfam: PF00188; SCP; 1.
CC PRINTS: PR00837; V5TPXLIKE.
CC PRODOM: PD000542; Allrgn_V5/TPx1; 1.
CC SMART: SM00198; SCP; 1.
CC PROSITE: PS01009; SCP_AG5_PRL_SCP_1; 1.
CC PROSITE: PS01010; SCP_AG5_PRL_SCP_2; 1.
CC Testis; Signal.
CC SIGNAL 1 22 POTENTIAL.
CC CHAIN 23 243 TESTIS-SPECIFIC PROTEIN TPX-1.
CC SEQUENCE 243 AA; 27605 MM; 6E707F569ACAA244 CMC64;
CC -----
Query Match 57.8%; Score 830; DB 1; Length 243;
Best Local Similarity 59.6%; Pred. No. 6.8e-64;
Matches 146; Conservative 39; Mismatches 58; Indels 2; Gaps 2;
CC -----
QY 14 MTLFVLLFLVAGLSPFANEDKDPATALLTOTOVOREIVNKHNLRAVSPPARNM 73
DB 1 MAMVOMLFEVALLLRSL-PLTEGKDPDTSLITNOLQVOREIVNKHNLRRSVNPTGSDI 59
QY 74 LKMEWKEAANAOKMAQNCYRHSNPKDRMTSLKCGENLWSSAPSSWSQAIOQMFDEY 133
DB 60 LKMEWSIQTATNAOKMAKCIHSHSSKDRKINIRCGENLWSSDPTLMSTYIOGWYEN 119
QY 134 NDFEGVGPRTPNNAVGHYTOVWYSSYLVCGNAYCPNOKLYKYVCYCPCAGNMNANR 193
DB 120 EDFYVGVGAK-PNSAVGHYTOVWYSSFKICGIAVCPNODLKYFYCHYCPMGNNYMK 178
QY 194 LYVPEOGAPCASPDCNDGCLTNGCKYEDLYSNCKSLKLTLCCKHQLVBDSCASCNC 253
DB 179 KSTRYQOSTPCASCPNCCNGLCTNSCDFELLSNCSLTKTSAGCKHLLTKCOATLC 238
QY 254 SNSIY 258
DB 239 EDKIH 243
CC -----
RESULT 6
AEG1_MOUSE STANDARD; PRT: 244 AA.
ID AEG1_MOUSE 003401;
AC 003401;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sperm-coating glycoprotein 1 precursor (SCP 1) (acidic epididymal
DE glycoprotein 1) (Cysteine-rich secretory protein-1) (Crisp-1).
GN AEG1 OR AEG-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE-Submandibular gland;
RA MEDLINE-93246016; PubMed-1301383;
RX Mizuki N., Kasahara M.;
RT "Mouse submandibular glands express an androgen-regulated transcript
RL encoding an acidic epididymal glycoprotein-like molecule."
RN Mol. Cell. Endocrinol. 89:25-32(1992).
RP [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Submandibular gland;
RX MEDLINE-93307144; PubMed-8319566;
RA Haendler B., Kratzschmar J., Theuring F., Schleuning M.D.;
RT "Transcripts for cysteine-rich secretory protein-1 (Crisp-1; DE/AGC)
RT and the novel related Crisp-3 are expressed under androgen control in
RT the mouse salivary gland."
RL Endocrinology 133:192-198(1993).
CC -1- FUNCTION: THIS PROTEIN IS SUPPOSED TO HELP SPERMATOZOA UNDERGO
CC FUNCTIONAL MATURATION WHILE THEY MOVE FROM THE TESTIS TO THE
CC DUCTUS DEFERENS.
CC -1- SUBCELLULAR LOCATION: STORED IN SECRETORY GRANULES OF GRANULAR
CC CONVOLUTED TUBULES CELLS.
CC -1- TISSUE SPECIFICITY: MAINLY FOUND IN THE CAUDA EPIDIDYMIS WHERE IT
CC IS SYNTHESIZED BY THE PRINCIPAL CELLS AND SECRETED INTO THE LUMEN.
CC BINDS TO THE HEADS OF SPERMATOZOON. ALSO EXPRESSED IN THE
CC SUBMANDIBULAR GLAND.
CC -1- DEVELOPMENTAL STAGE: EXPONENTIAL INCREASE BETWEEN DAYS 25 AND 30
CC AFTER BIRTH.
CC -1- INDUCTION: By androgens.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC -----
CC EMBL: M92849; AAA37185.1; -.
CC EMBL: L05559; AAA37460.1; -.
CC PIR: A49202; AAA37460.1; -.
CC MGD: MGI:102553; Aeg1.
CC InterPro: IPR001283; Allrgn_V5/TPx1.
CC Pfam: PF00188; SCP; 1.
CC PRINTS: PR00837; V5TPXLIKE.
CC PRODOM: PD000542; Allrgn_V5/TPx1; 1.
CC SMART: SM00198; SCP; 1.
CC PROSITE: PS01009; SCP_AG5_PRL_SCP_1; 1.
CC PROSITE: PS01010; SCP_AG5_PRL_SCP_2; 1.
CC Sperm; Glycoprotein; Signal.
CC SIGNAL 1 19
CC CHAIN 20 244 SPERM-COATING GLYCOPROTEIN 1.
CC CARBOHYD 145 145 N-LINKED (GLCNAC. ) (POTENTIAL).
CC FT 244
CC SEQUENCE 244 AA; 27679 MM; D00DD0348F85781F CMC64;
CC -----
Query Match 53.4%; Score 766.5; DB 1; Length 244;
Best Local Similarity 55.1%; Pred. No. 1.8e-58;
Matches 135; Conservative 39; Mismatches 70; Indels 1; Gaps 1;
CC -----
QY 14 MTLFVLLFLVAGLSPFANEDKDPATALLTOTOVOREIVNKHNLRAVSPPARNM 73
DB 1 MAMVOMLFEVALLLRSL-PLTEGKDPDTSLITNOLQVOREIVNKHNLRRSVNPTGSDI 59
QY 74 LKMEWKEAANAOKMAQNCYRHSNPKDRMTSLKCGENLWSSAPSSWSQAIOQMFDEY 133
DB 61 LKMEWKEAANAOKMAQNCYRHSNPKDRMTSLKCGENLWSSAPSSWSQAIOQMFDEY 120
QY 134 NDFEGVGPRTPNNAVGHYTOVWYSSYLVCGNAYCPNOKLYKYVCYCPCAGNMNANR 193
DB 121 KDLVYDVGKPDSDVGHYTOVWYSSYLVCGNAYCPNOKLYKYVCYCPCAGNMNANR 179
QY 194 LYVPEOGAPCASPDCNDGCLTNGCKYEDLYSNCKSLKLTLCCKHQLVBDSCASCNC 253

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Db 180 LPTYPAGEPCASCPDHCEDGLCTNSCGHEDKYTNCKTKLKKMLSCSEHELLKGCATGCLC 239
OY 254 SNSIT 258
Db 240 ECKIH 244

RESULT 7
AEG_RAT
ID AEG_RAT STANDARD: PRT: 246 AA.
AC P12020;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sperm-coating glycoprotein precursor (SCP) (Acidic epididymal
glycoprotein) (Protein D) (Protein E) (Protein IV) (Staloprotein)
DE (32 kDa epididymal protein).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-Epididymis;
RX MEDLINE=87053995; PubMed=3780731;
RA Brooks D.E., Means A.R., Wright E.J., Singh S.P., Tiver K.K.;
RT "Molecular cloning of the cDNA for androgen-dependent sperm-coating
glycoproteins secreted by the rat epididymis."
RL Eur. J. Biochem. 161:13-18(1986).
RN (12)
RP SEQUENCE FROM N.A.
RX MEDLINE=89039913; PubMed=2460753;
RA Charrest N.J., Joseph D.R., Wilson E.M., French F.S.;
RT "Molecular cloning of complementary deoxyribonucleic acid for an
androgen-regulated epididymal protein: sequence homology with
metalloproteins."
RL Mol. Endocrinol. 2:999-1004(1988).
CC -1- FUNCTION: THIS PROTEIN IS SUPPOSED TO HELP SPERMATOZOEA UNDERGO
FUNCTIONAL MATURATION WHILE THEY MOVE FROM THE TESTIS TO THE
DUCTUS DEFERENS.
CC -1- INDUCTION: By androgens.
CC -1- MISCELLANEOUS: SCP IS AN ANDROGEN-DEPENDENT PROTEIN, WHICH IS
SECRETED BY THE EPIDIDYMAL EPITHELIUM AND THEN BECOMES ASSOCIATED
WITH THE SPERM SURFACE. TWO MAJOR VARIANT PROTEIN D AND E DIFFER
FROM EACH OTHER BY THEIR CARBOHYDRATE SIDE CHAINS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC -----
DR EMBL: X04643; CA28304.1;
DR EMBL: M31173; AAB59716.1;
DR PIR: A24609; A24609.
DR PIR: A40918; A40918.
DR InterPro: IPR001283; Allrgn_V5/TPX1.
DR Pfam: PF00188; SCP_1.
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/TPX1; 1.
DR SMART: SM00198; SCP_1.
DR PROSITE: PS01009; SCP_AG5_PRL_SC7_1; 1.
DR PROSITE: PS01010; SCP_AG5_PRL_SC7_2; 1.
KW Sperm; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 246 SPERM-COATING GLYCOPROTEIN.
FT MOD_RES 20 20 BLOCKED (POTENTIAL).
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 246 AA: 27847 MW; 585207C7CF7CE9D1 CRC64.

Query Match 52.6%; Score 755.5; DB 1; Length 246;
Best Local Similarity 55.1%; Pred. No. 1.6e-57;
Matches 136; Conservative 35; Mismatches 73; Indels 3; Gaps 2;

OY 14 MTLFPVLLFLVAGLPSF--PANEDKDPATFALLTTOTVOGREIYNKHNELRAVSPAR 71
Db 1 MALMLVLLFLAAVLPSPSTQDTTDEMIDRLNLTSTKLSEVDEIINKHQRLRTSPGS 60
OY 72 NNLKMKMKKKAANKANOKNANOCNRYHSNPKDMTSLKCGENLYMSAPSWSQAIOSPFD 131
Db 61 DLRLVEMDHDAIVNAOKNANRCITNHSPLQHTTTLKCGENLFMANYPASMSVYQDMYD 120
OY 132 EYNDFGFGVGPRTPAVVGHYTOVWVSSYLVCGNAYCPNOKVLYKYYVCYCPAGNMA 191
Db 121 ESLDFVFGFGPKKVGKGYHYTOVWVNSFLVACGVAECPDP--LKIFYVCHYCGGHVY 179
OY 192 NRLVYPTGEGAPCASCPCNDGDLCTNGCKYEDLYSNCKSLKLLITCKHQLVRSCKASC 251
Db 180 GLYSPYTEGECDCSPGNCEDGLCTNSCEYEDNYSNCGDLKKVYSCDPLLEKGCASC 239
OY 252 NCSNIT 258
Db 240 FLEDKIH 246

RESULT 8
HELO_HELHO
ID HELO_HELHO STANDARD: PRT: 242 AA.
AC Q91055;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Helothermine precursor (HLTX).
CC Heloderma horridum horridum (Mexican beaded lizard).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Lepidosauria; Squamata; Scleroglossa; Anguilliformes; Helodermatidae;
CC Heloderma.
CC NCBI_TaxID=8552;
RN (1)
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE-Salivary gland;
RX MEDLINE=95375162; PubMed=7647234;
RA Morrissette J., Kraetzschmar J., Haendler B., El-Hayek R.,
RA Mochica-Morales J., Martin B.M., Patel J.R., Moss R.L.,
RA Schenking W.-D., Coronado R., Posaani L.D.;
RT "Primary structure and properties of helothermine, a peptide toxin
that blocks ryanodine receptors."
RL Biophys. J. 68:2280-2288(1995).
RN (12)
RP SEQUENCE OF 20-39, AND CHARACTERIZATION.
RX TISSUE-Venom;
RX MEDLINE=90260878; PubMed=1693019;
RA Mochica-Morales J., Martin B.M., Posaani L.D.;
RT "Isolation and characterization of helothermine, a novel toxin from
Heloderma horridum horridum (Mexican beaded lizard) venom."
RL Toxicon 28:299-309(1990).
CC -1- FUNCTION: Toxin that blocks ryanodine receptors. It is toxic to
mice; it causes lethargy, partial paralysis of rear limbs and
lowering of body temperature.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Produced by the venomous gland.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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 CC -----  
 DR EMBL: U13619; AAC59730.1; -.  
 DR InterPro: IPR001283; Allrgn\_V5/TPx1.  
 DR Pfam: PF00188; SCP: 1.  
 DR PRINTS: PR00837; VSTPXLKE.  
 DR ProDom: PD000542; Allrgn\_V5/TPx1; 1.  
 DR SMART: SM00198; SCP: 1.  
 DR PROSITE: PS01009; SCP\_AGS\_PRL\_SCT\_2; FALSE\_NEG.  
 DR PROSITE: PS01010; SCP\_AGS\_PRL\_SCT\_2; FALSE\_NEG.  
 DR Calcium channel inhibitor; Neurotoxin; Toxin; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 242  
 FT SEQUENCE 242 AA; 27493 MW; 0E183FC2F925DF3C CRC64;  
 SO  
 Query Match 46.8%; Score 671.5; DB 1; Length 242;  
 Best Local Similarity 50.2%; Pred. No. 2.3e-50;  
 Matches 123; Conservative 31; Mismatches 86; Indels 5; Gaps 3;  
 QY 14 MTLPPVLLFLVAGLLSPFANEDKDPATFALLTQTOYQREIVKHNELRAVSPPARNM 73  
 Db 1 MILSLVLCIAAMLHOS---EGEASPKLPGMLTSPDOQTETDKNHNLRIIVEPTASNM 57  
 QY 74 LKMEMNKEAANAOKWANKNOCYRHSNPKDR-MTSLKCGENTLYSSAPSSQAIOSWFE 132  
 Db 58 LKMTMSNKIAGNAORASNAOCLEHTSKERTIDGEGENLFPSAPYATWYAIQNMWDE 117  
 QY 133 YNDEDFGCPKTPNANVGHITQVWYSSYLVCGCNATCPNOKLVLYYYCQCPAGNMAN 192  
 Db 118 RKYRFENYGPAAQNVMMIGHITQVWYRSEYEGCAIAYCPDQPTKYXYVCQCPGSGNIRS 177  
 QY 193 RLYVPEEGAPCASPDCDGLCTNGCKYEDLYSNCKSLTLTLCKHQLRDSCAKSN 252  
 Db 178 RKYRFYSIGPCGDCPDACDGLCTNPKQNDYINPCDLKQYCGCHPMKD-CMATCK 236  
 QY 253 CSNSI 257  
 Db 237 CLTEI 241  
 RESULT 9  
 AEG2\_MOUSE STANDARD; PRT; 241 AA.  
 ID AEG2\_MOUSE  
 AC 003402;  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Sperm-coating glycoprotein 2 precursor (SCP 2) (Acidic epididymal  
 DE glycoprotein 2) (Cysteine-rich secretory protein-3) (Crisp-3).  
 GN AEG2 OR AEG-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RX MEDLINE=93246016; PubMed=1301383;  
 RA Mizuki N., Kasahara M.;  
 RT "Mouse submandibular glands express an androgen-regulated transcript  
 RT encoding an acidic epididymal glycoprotein-like molecule."  
 RL Mol. Cell. Endocrinol. 89:25-32(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Submandibular gland;  
 RX MEDLINE=93307144; PubMed=8319566;  
 RA Haendler B., Kratzschmar J., Theuring F., Schleuning W.D.;  
 RT "Transcripts for cysteine-rich secretory protein-1 (CRISP-1; DE/AGC)  
 RT and the novel related CRISP-3 are expressed under androgen control in  
 RT the mouse salivary gland."  
 RL Endocrinology 133:192-198(1993).

CC -1- FUNCTION: THIS PROTEIN IS SUPPOSED TO HELP SPERMATOZOA UNDERGO  
 CC FUNCTIONAL MATURATION WHILE THEY MOVE FROM THE TESTIS TO THE  
 CC DUCTUS DEFERENS.  
 CC -1- SUBCELLULAR LOCATION: STORED IN SECRETORY GRANULES OF GRANULAR  
 CC CONVOLUTED TUBULES CELLS.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN SUBMANDIBULAR GLAND.  
 CC -1- DEVELOPMENTAL STAGE: EXPONENTIAL INCREASE BETWEEN DAYS 25 AND 30  
 CC AFTER BIRTH.  
 CC -1- INDUCTION: BY androgens.  
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
 CC INSECTS AG3/AG5; FUNGI SCT/SCI4 AND PLANTS PR-1.  
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 CC -----  
 DR EMBL: M92850; AAA37186.1; -.  
 DR EMBL: L05560; AAA37461.1; -.  
 DR PIR: B49202; B49202.  
 DR MGD: MGI:102552; Aeg2.  
 DR InterPro: IPR001283; Allrgn\_V5/TPx1.  
 DR Pfam: PF00188; SCP: 1.  
 DR PRINTS: PR00837; VSTPXLKE.  
 DR ProDom: PD000542; Allrgn\_V5/TPx1; 1.  
 DR SMART: SM00198; SCP: 1.  
 DR PROSITE: PS01009; SCP\_AGS\_PRL\_SCT\_1; 1.  
 DR PROSITE: PS01010; SCP\_AGS\_PRL\_SCT\_2; 1.  
 DR Sperm; Glycoprotein; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 241  
 FT CARBOHYD 118 118  
 FT CARBOHYD 132 132  
 FT CARBOHYD 175 175  
 FT SEQUENCE 241 AA; 27314 MW; D903788B4E4001EF CRC64;  
 SO  
 Query Match 43.0%; Score 617.5; DB 1; Length 241;  
 Best Local Similarity 48.4%; Pred. No. 9.1e-46;  
 Matches 118; Conservative 40; Mismatches 79; Indels 7; Gaps 3;  
 QY 14 MTLPPVLLFLVAGLLSPFANEDKDPATFALLTQTOYQREIVKHNELRAVSPPARNM 73  
 Db 1 MALMLVFLFLAAVLPPLSLQDNSQENSLKSTKSVQETIVKHNLRKRVSPSGSDL 60  
 QY 74 LKMEMNKEAANAOKWANKNOCYRHSNPKDRMTSLKCGENTLYSSAPSSQAIOSWFE 133  
 Db 61 LKMEMNDAQVNAOQDRKCFESHSPLELRTNLKCGENLFMSYLVPMWSVIGWNES 120  
 QY 134 NDFPFGCPKTPNANVGHITQVWYSSYLVCGCNATCPNOKLVLYYYCQCP----AGN 189  
 Db 121 KGLIFGVGPKNQVSVGHITQVWYKSNQVAGVABCP-ENPLRYFYCRCPVLNLSGH 179  
 QY 190 WANRLVPEEGAPCASPDCDGLCTNGCKYEDLYSNCKSLTLTLCKHQLRDSCAK 249  
 Db 180 YPSRPLYATRAFCASCPCDCEGLCTKSCQYKDMSEWCK--RLLEYVCKHPGLKKRCLA 237  
 QY 250 SCNC 253  
 Db 238 TCQC 241  
 RESULT 10  
 CRVP-TRIMU STANDARD; PRT; 183 AA.  
 ID CRVP-TRIMU  
 AC P79845;  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cysteine-rich venom protein precursor (CRVP).  
 DE Trimeresurus mucrosquamatus (Taiwan habu).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidostei; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Protobothrops.
OX NCBI_TaxID=103944;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-Venom gland;
RX MEDLINE=97385768; PubMed=9241782;
RA Chang T.-Y., Mao S.-H., Guo Y.-W.;
RT "Cloning and expression of a cysteine-rich venom protein from
RT Trimeresurus mucrosquamatus (Taiwan habu).";
RL Toxicon 35:879-888(1997).
CC -1- FUNCTION: May be a toxin that blocks ryanodine receptors.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Produced by the venomous gland.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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CC -----
DR EMBL: U59447; AAB48565.1; -
DR InterPro: IPR001283; Allrgn_V5/TPx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/TPx1; 1.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01009; SCP_AGS_PRL_SC7_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SC7_2; 1.
DR Calcium channel inhibitor; Neurotoxin; Toxin; Signal.
KM SIGNAL 1 21
FT CHAIN 1 21
SQ SEQUENCE 183 AA; 20378 MW; 50224DBE92A64930 CRC64;

Query Match
Best Local Similarity 51.4%; Pred. No. 2,6e-40; Length 183;
Matches 94; Conservative 23; Mismatches 64; Indels 2; Gaps 2;

OY 76 MEMNKAANAOQKMANOCYRHSNPKDRMT-SLKCGENTLYMSSAPSSOAIOSMFDEVN 134
DB 1 MEMYPPAANAERMAKRCLESHSRSDSRVIGCKGCEINIMSPYAKWIDIHANMGEYK 60
OY 135 DFDFGVGPTPPNAVVGHTYQVWYSSYLVGCGNAYCPNOKVLYKYVYCOYCPAGNNANRL 194
DB 61 DERKYGAVPSPNAAHTGYQIOWYKYSRGCAAYCPSSK-YRYFYVCOYCPAGNNIGKT 119
OY 195 YPYEYGACAPSCPNDCDGLCTNGCKYEDLYSNCKSLKTLTKCKQLVAVDSCKASCNC 254
DB 120 APTPTSGPPCGDPCSDCDGLCTNCTOETNTSNCSNLVQSSCDQNNMKTCPASCFCQ 179
OY 255 NSI 257
DB 180 NKI 182

RESULT 11
CSRL_HUMAN STANDARD; PRT; 249 AA.
AC PS4107; 013248; 000698; 014082;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cysteine-rich secretory protein-1 precursor (Acidic epididymal
DE glycoprotein homolog) (AEG-like protein) (ARP).
GN AEG1 OR CRISP-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), AND SEQUENCE OF 22-41.
RX MEDLINE=96270732; PubMed=8665901;
RA Kretzschmar J., Haendler B., Eberspaecher U., Roostermann D.,
RA Donner P., Schleuning W.-D.;
RT "The human cysteine-rich secretory protein (CRISP) family. Primary
RT structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3.";
RL Eur. J. Biochem. 236:827-836(1996).
RN (2)
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RX MEDLINE=96103955; PubMed=8543280;
RA Hayashi M.;
RT "Analysis of the human acidic epididymal glycoprotein-like molecule:
RT isolation of cDNA and tissue localization.";
RL HOKKAIDO IGAKU ZASSHI 70:743-753(1995).
RN (3)
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND CHARACTERIZATION.
RX MEDLINE=96435914; PubMed=8838800;
RA Hayashi M., Fujimoto S., Takano H., Ushiki T., Abe K., Ishikura H.,
RA Yoshida M.C., Kirchhoff C., Ishibashi T., Kasahara M.;
RT "Characterization of a human glycoprotein with a potential role in
RT sperm-egg fusion: cDNA cloning, immunohistochemical localization,
RT and chromosomal assignment of the gene (AEG1).";
RL Genomics 32:367-374(1996).
CC -1- FUNCTION: MAY HAVE A ROLE IN SPERM-EGG FUSION AND MATURATION.
CC -1- SUBCELLULAR LOCATION: LOCATED IN THE LUMEN AND EPITHELIUM OF
CC DISTAL DUCTUS EPIDIDYMUS AND EPIDIDYMAL DUCTS, AND ON THE
CC POSTACROSOMAL REGION OF THE SPERM HEAD.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a
CC short form/CRISP-1 delta; may be produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: CAPUT, CORPUS, AND CAUDA REGIONS OF THE
CC EPIDIDYMUS. THE DUCTUS DEFERENS, SPERM, AND SEMINAL PLASMA.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC -----
DR EMBL: X95237; CA64524.1; -
DR EMBL: X95238; CA64525.1; -
DR EMBL: 680310; AAB55889.1; -
DR EMBL: D38451; BAA07483.1; -
DR GeneW: HGNC:304; AEG1.
DR MIM: 601193; -
DR InterPro: IPR001283; Allrgn_V5/TPx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/TPx1; 1.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01009; SCP_AGS_PRL_SC7_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SC7_2; 1.
DR Glycoprotein; Signal; Multigene family; Alternative splicing.
KM SIGNAL 1 21
FT CHAIN 1 21
FT CARBOHYD 22 249
FT VARSPLIC 178 178
FT VARSPLIC 179 249
FT CONFLICT 22 22
FT CONFLICT 97 97
SQ SEQUENCE 249 AA; 28481 MW; 85BED3DEAD62A9C CRC64;

Query Match
Best Local Similarity 36.9%; Score 529.5; DB 1; Length 249;
Matches 111; Conservative 26; Mismatches 100; Indels 7; Gaps 5;

OY 20 LFLVAG--LLP--SEPNADKDPATFALLTTOGVQREIVNKHNEIRRAVSPARRMVK 75
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DB 6 LFLVLAACLLPMLSMKKKSARD-QFNKLVTDLNVQDEIYNHINALRRVPPASNMK 64
QY 76 MEANKEAANQKWAQNCNRYHSPKRD-RMTSLKCGENTLYNSAPSSWSQAIOGFDEYN 134
DB 65 MSMESEAAQNAIRFSKYCDMTESNPLERLPNFCGEMHMTSPVMSVSIQVWYSSST 124
QY 135 DFDGCVGPKRTNAV-VGHTYQVWYSSYLVCAGNAYCNOVYLVKYYVQYCPAGNMNR 193
DB 125 SFKGEWTTTDDITTDYHTQIWMATSYLCAIASCROGSPRLYVCHYCHEGNDPET 184
QY 194 LYVPEOGAPCASPDCNDGCLCTNGCKYEDLYSNCKSLKLTLCCKHQLVADSCASCNC 253
DB 185 KNEPKYGVPCDAGCSNCEKLTNPCTIYDEYFDGDIQVHYLCCNHTLTFCKATCLC 244
QY 254 SNSI 257
DB 245 DTEI 248

RESULT 12
GLIP_HUMAN STANDARD: PRT: 266 AA.
ID GLIP_HUMAN
AC P48060: 015409:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glioma pathogenesis-related protein (GLIPR) (RTVP-1 protein).
GN GLIPR OR RTVP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Glial tumor:
RX MEDLINE=97128816; PubMed=8973356;
RA Rich T., Chen P., Furman F., Huiyuh N., Israel M.A.;
RT "RTVP-1, a novel human gene with sequence similarity to genes of
RT diverse species, is expressed in tumor cell lines of glial but not
RT neuronal origin.";
RL Gene 180:125-130(1996).
RN [2]
RP SEQUENCE OF 11-266 FROM N.A.
RX MEDLINE=95331646; PubMed=7607567;
RA Murphy E.V., Zhang Y., Zhu W., Biggs J.;
RT "The human glioma pathogenesis-related protein is structurally
RT related to plant pathogenesis-related proteins and its gene is
RT expressed specifically in brain tumors.";
RL Gene 159:131-135(1995).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=98151500; PubMed=9482873;
RA Sayperski T., Fernandez C., Mumenthaler C., Wuehrlich K.;
RT "Structure comparison of human glioma pathogenesis-related protein
RT GLIPR and the plant pathogenesis-related protein Pla indicates a
RT functional link between the human immune system and a plant defense
RT system.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:2262-2266(1998).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE HUMAN BRAIN TUMOR,
CC GLOBLASTOMA MULTIFORM/ASTROCYTOMA, BUT NEITHER IN NORMAL FETAL
CC OR ADULT BRAIN TISSUE, NOR IN OTHER NERVOUS SYSTEM TUMORS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -1- This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC EMBL: X91911; CAA63005.1;

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DR EMBL: U16307; AAA82731.1;
DR HSSP: P04284; ICFE.
DR MIM: 602692;
DR InterPro: IPR001283; Allrgn_V5/TPX1.
DR Pfam: PF00188; SCP.1.
DR PRINTS: PR00837; V5TPX1IKE.
DR ProDom: PD000542; Allrgn_V5/TPX1.1.
DR SMART: SM00198; SCP.1.
DR PROSITE: PS01009; SCP_AG5_PRL_SC7_1; 1.
DR PROSITE: PS01010; SCP_AG5_PRL_SC7_2; 1.
FT CONFLICT 125 125 D->N (IN REF. 2).
FT CONFLICT 209 266 RQDQVARYTSVYPGPITPRNRRTSLFLIVSVILLISV
FT T (IN REF. 2).
SQ SEQUENCE 266 AA; 30342 MW; C04378085EFB287A CRC64;

Query Match 22.88; Score 328; DB 1; Length 266;
Best Local Similarity 34.98; Pred. No. 5.2e-21;
Matches 81; Conservative 34; Mismatches 71; Indels 46; Gaps 12;

QY 9 LETTAMTLFVLLFL-----VAGLSPFPANEDKDPATFALLTQTQVQREIVKHNELR 63
DB 1 MRTLATIAMVSVFVSNYSHTANILPDI-ENED-----FIKCVIHNKFR 45
QY 64 RAVSPARNMLKMEKNKEAANAQKMANOCNRYRS---NPKDRM-----TSLKCGENTLYMS 116
DB 46 SEVKPTASDMLYMWDPALAOIAKAMASNCQFSNTRLKPKHKLHPNTSL--GENIWTG 103
QY 117 SAP-SSMSQAIOQSFDEYNDFGVGPKRTNAVYGHITQVWYSSYLVCAGNATCPNOKY 175
DB 104 SVPIFSVSSALTNNWYDEIDYDFKT--RICKKVGHTQVWMAQSYKGCAYQCP--KV 159
QY 176 LKY-----YVCOYCPAGMANRLVYVPEOGAPCASPDCPN--CDGCLCTN 218
DB 160 SGFPAISNGAIFICNYPGGMYPF---WPKRGATCSACPNKDCIDNLGVN 208

RESULT 13
ASP_ANCCA STANDARD: PRT: 424 AA.
ID ASP_ANCCA
AC Q16937;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ancylostoma secreted protein precursor.
GN ASP.
OS Ancylostoma caninum (dog hookworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongyloida;
OC Ancylostomatoidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
OX NCBI_TaxID=29170;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96215086; PubMed=8636085;
RA Haddon J.M., Jones B.F., Hoffman D.R., Hotez P.J.;
RT "Cloning and characterization of Ancylostoma-secreted protein, A
RT novel protein associated with the transition to parasitism by
RT infective hookworm larvae.";
RL J. Biol. Chem. 271:6672-6678(1996).
CC -1- FUNCTION: ASSOCIATED WITH THE TRANSITION TO PARASITISM BY
CC INFECTIVE HOOKWORM LARVAE.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -1- This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC EMBL: U26187; AAC47001.1;
DR HSSP: P04284; ICFE.

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DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/Tpx1; 2.
DR SMART: SM00198; SCP; 2.
DR PROSITE: PS01009; SCP_AGS_PRL_SCT_1; FALSE_NEG.
DR PROSITE: PS01010; SCP_AGS_PRL_SCT_2; FALSE_NEG.
KM SIGNAL.
FT CHAIN 1 18 POTENTIAL.
FT SEQUENCE 19 424 ANCYLOSTOMA SECRETED PROTEIN.
SQ SEQUENCE 424 AA: 45735 MW: 48082953D3035F9 CRC64;

Query Match
Best Local Similarity 31.1%; Score 274; DB 1; Length 424;
Matches 68; Conservative 37; Mismatches 70; Indels 44; Gaps 9;

OY 29 PSFPANEKDAFTALTTOTOVOREIYNKHNELRAV-----SPARNMLKM 76
DB 218 PDVPEPTNOCCPSMTGMTDS---VRDTFLSVHNEFRSSVARGLEPDALGNAKAKMLKM 274
OY 77 ENKKEAANAOKMANOCNVRHNSPNKDRMTSLKCGENLYMSSA-----PSMSQAIOISWPD 131
DB 275 VYDCEVEASAIRHGKNCYQSHGEDRP---GLGENITYKTVLAKDKNAKAKASQMLMWN 331
OY 132 EYNDEFGVGPKT-----PNAVGHYTOVWVYSSYLVCGNAYCPNOKVLYKYYVC 182
DB 332 ELK--EFGVGPSNVLTTLALMNRGMQIGHYIOMANDTYTKLGCAVVFCDFT----FGVC 385
OY 183 OYCPAGNANRLVPEEGCAPCASCPCD-----NCDGLCT 217
DB 386 OYGPGENYWG--HVITYMGOPCSCSPGATCSVTEGLCS 422

RESULT 14
V521_VESCR STANDARD: PRT: 202 AA.
ID V521_VESCR
AC P35781;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Venom allergen 5.01 (Antigen 5-1) (AG5-1) (Allergen Vesp c 5.01) (Vesp c V.01).
OS Vespa crabro (European hornet).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7445;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=94044316; PubMed=8227862;
RA Hoffman D. R.;
RT "Allergens in Hymenoptera venom. XXV: The amino acid sequences of antigen 5 molecules and the structural basis of antigenic cross-reactivity."
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SCT/SC14 AND PLANTS PR-1.
DR PIR: G44522; G44522.
DR PIR: G44583; G44583.
DR HSSP: P04284; ICPE.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01009; SCP_AGS_PRL_SCT_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SCT_2; 1.
KM Venom; Allergen.
FT DISULFID 4 16 BY SIMILARITY.
FT DISULFID 8 101 BY SIMILARITY.
FT DISULFID 26 94 BY SIMILARITY.
FT DISULFID 168 185 BY SIMILARITY.

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SQ SEQUENCE 202 AA: 22722 MW: EDEB39905B598997 CRC64;

Query Match
Best Local Similarity 18.7%; Score 269; DB 1; Length 202;
Matches 61; Conservative 23; Mismatches 60; Indels 20; Gaps 5;

OY 45 LTTOTVOREIYNKHNELRAVS-----PPARNMLKMEKNKEAANAOKMANO 92
DB 36 LTKQENL--ELIKQHNFEPRKAVARGLETRGNPGPPAKSMNTLVNDELAQIAQVMANO 93
OY 93 CNYRHSNPKDRMTSLKCGENLYMSSAPS-----SMSQAIOISWPDENDFGCGPKTPNAV 148
DB 94 CNYGHDCNRN--SAKYSVQONIAEGSTADNFGSVSNMVMKMEDEKDYQYG--SPRNKLK 151
OY 149 VGHYTOVWVYSSYLVCGNAYCPNOKVLYKYYVCYCPAGNMAN 192
DB 152 VGHYTOVMATKKEIGCGSIKIENGWHRHYLVCAVGRAGNYGN 195

RESULT 15
V522_VESCR STANDARD: PRT: 202 AA.
ID V522_VESCR
AC P35782;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Venom allergen 5.02 (Antigen 5-2) (AG5-2) (Allergen Vesp c 5.02) (Vesp c V.02).
OS Vespa crabro (European hornet).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7445;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=94044316; PubMed=8227862;
RA Hoffman D. R.;
RT "Allergens in Hymenoptera venom. XXV: The amino acid sequences of antigen 5 molecules and the structural basis of antigenic cross-reactivity."
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SCT/SC14 AND PLANTS PR-1.
DR PIR: H44522; H44522.
DR PIR: H44583; H44583.
DR HSSP: P04284; ICPE.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01009; SCP_AGS_PRL_SCT_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SCT_2; 1.
KM Venom; Allergen.
FT DISULFID 4 16 BY SIMILARITY.
FT DISULFID 8 101 BY SIMILARITY.
FT DISULFID 26 94 BY SIMILARITY.
FT DISULFID 168 185 BY SIMILARITY.
SQ SEQUENCE 202 AA: 22781 MW: B710E9198413F547 CRC64;

Query Match
Best Local Similarity 18.5%; Score 265; DB 1; Length 202;
Matches 60; Conservative 24; Mismatches 60; Indels 20; Gaps 5;

OY 45 LTTOTVOREIYNKHNELRAVS-----PPARNMLKMEKNKEAANAOKMANO 92
DB 36 LTKQENL--ELIKQHNFEPRKAVARGLETRGNPGPPAKSMNTLVNDELAQIAQVMANO 93
OY 93 CNYRHSNPKDRMTSLKCGENLYMSSAPS-----SMSQAIOISWPDENDFGCGPKTPNAV 148
DB 94 CNYGHDCNRN--SAKYSVQONIAEGSTADNFGSVSNMVMKMEDEKDYQYG--SPRNKLK 151

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Oy 149 VGHYTOVWYSSYLVCNAYCPNOKYVKYXYVCQYCPAGNMAN 192  
| | | | | : | | | : | | | | |  
Db 152 VGHYTOVWMAKKEICGSEDYIEDGWHRRHYLCNNGSPAGNVMN 195

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Job time : 21.3258 secs